S, Huff.

1642 #7

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> **This Raw Listing contains the General Information Section and up to the first 5 pages.**

```
 1                                        SEQUENCE LISTING
 2
 3     (1)     General Information:
 4
 5          (i) APPLICANT: Holmes, Stephen D.
 6                         Gross, Mitchell S.
 7                         Sylvester, Daniel R.
 8
 9         (ii) TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
10              Treatment of IL4 Mediated Disorders
11
12        (iii) NUMBER OF SEQUENCES: 58
13
14         (iv) CORRESPONDENCE ADDRESS:
15              (A) ADDRESSEE: SmithKline Beecham Corporation
16              (B) STREET: Corporate Intellectual Property, UW2220 - 709
17                  Swedeland Rd.
18              (C) CITY: King of Prussia
19              (D) STATE: PA
20              (E) COUNTRY: USA
21              (F) ZIP: 19406-2799
22
23          (v) COMPUTER READABLE FORM:
24              (A) MEDIUM TYPE: Floppy disk
25              (B) COMPUTER: IBM PC compatible
26              (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27              (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
28
29         (vi) CURRENT APPLICATION DATA:
30              (A) APPLICATION NUMBER: 09/426,814
31              (B) FILING DATE:
32              (C) CLASSIFICATION:
33
34        (vii) PRIOR APPLICATION DATA:
35              (A) APPLICATION NUMBER: 08/612,929
36              (B) FILING DATE:
37
38              (A) APPLICATION NUMBER: US 08/136,783
39              (B) FILING DATE: 14-OCT-1993
40
41       (viii) ATTORNEY/AGENT INFORMATION:
42              (A) NAME: Sutton, Jeffrey A.
43              (B) REGISTRATION NUMBER: 34,028
44              (C) REFERENCE/DOCKET NUMBER: P50186-2
45
46         (ix) TELECOMMUNICATION INFORMATION:
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```
47                    (A) TELEPHONE: (215) 270-5024
48                    (B) TELEFAX: (215) 270-5090
49
50
51
52    (2) INFORMATION FOR SEQ ID NO:1:
53
54          (i) SEQUENCE CHARACTERISTICS:
55                (A) LENGTH: 396 base pairs
56                (B) TYPE: nucleic acid
57                (C) STRANDEDNESS: double
58                (D) TOPOLOGY: unknown
59
60          (ii) MOLECULE TYPE: cDNA
61
62          (ix) FEATURE:
63                (A) NAME/KEY: CDS
64                (B) LOCATION: 1..396
65
66
67
68
69
70
71          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
72
73    ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTG CTC TGG GTT CCA        48
74    Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
75     1               5                   10                  15
76
77    GGC TCC ACT GGT GAC ATT GTG CTG ACC CAA TCT CCA GCT TCT TTG GCT        96
78    Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
79                20                  25                  30
80
81    GTG TCT CTA GGG CAG AGG GCC ACC ATC TCC TGC AAG GCC AGC CAA AGT       144
82    Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
83            35                  40                  45
84
85    GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAC CAA CAG AAA CCA       192
86    Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
87         50                  55                  60
88
89    GGA CAG CCA CCC AAA CTC CTC ATC TAT GCT GCA TCC AAT CTA GAA TCT       240
90    Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser
91     65                  70                  75                  80
92
93    GGG ATC CCA GCC AGG TTT AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC       288
94    Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
95                85                  90                  95
96
97    CTC AAC ATC CAT CCT GTG GAG GAG GAG GAT GCT GCA ACC TAT TAC TGT       336
98    Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
99                100                 105                 110
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100
101    CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GGC ACC AAG CTG        384
102    Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
103            115                 120                 125
104
105    GAA ATC AAA CGG                                                        396
106    Glu Ile Lys Arg
107        130
108
109
110    (2) INFORMATION FOR SEQ ID NO:2:
111
112            (i) SEQUENCE CHARACTERISTICS:
113                  (A) LENGTH: 132 amino acids
114                  (B) TYPE: amino acid
115                  (D) TOPOLOGY: linear
116
117            (ii) MOLECULE TYPE: protein
118
119            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
120
121    Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
122     1               5               10                  15
123
124    Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
125            20                  25                  30
126
127    Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
128            35                  40                  45
129
130    Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
131        50                  55                  60
132
133
134    Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser
135     65                  70                  75                  80
136
137    Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
138                    85                  90                  95
139
140    Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
141                100                 105                 110
142
143    Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
144            115                 120                 125
145
146    Glu Ile Lys Arg
147        130
148
149
150    (2) INFORMATION FOR SEQ ID NO:3:
151
152            (i) SEQUENCE CHARACTERISTICS:
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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/426,814

INPUT SET: S36192.raw

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153              (A) LENGTH: 483 base pairs
154              (B) TYPE: nucleic acid
155              (C) STRANDEDNESS: double
156              (D) TOPOLOGY: unknown
157
158          (ii) MOLECULE TYPE: cDNA
159
160          (ix) FEATURE:
161              (A) NAME/KEY: CDS
162              (B) LOCATION: 64..483
163
164          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
165
166  GAATTCGCGG CCGCTATGCA GGGACAATCA GCAGCAGCAA TGAGGAAGTA AGCCTGTGCA        60
167
168  GAT ATG AAC AGG CTT ACT TCC TCA TTG CTG CTG CTG ATT GTC CCT GCA       108
169      Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Leu Ile Val Pro Ala
170       1               5                  10                  15
171
172  TAT GTC CTG TCC CAG GTT ACT CTG AAA GAG TCT GGC CCT GGG ATA TTG       156
173  Tyr Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu
174                  20                  25                  30
175
176  CAG CCC TCC CAG ACC CTC AGT CTG ACT TGT TCT TTC TCT GGG TTT TCA       204
177  Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser
178              35                  40                  45
179
180  CTG AGC ACT TCT GGT ATG GGT GTG AGC TGG ATT CGT CAG CCT TCA GGA       252
181  Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly
182          50                  55                  60
183
184  AAG GGT CTG GAG TGG CTG GCA CAC ATT TAC TGG GAT GAT GAC AAG CGC       300
185  Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg
186      65                  70                  75
187
188  TAT AAC CCA TCC CTG AAG AGC CGG CTC ACA ATC TCC AAG GAT ACC TCC       348
189  Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
190   80                  85                  90                  95
191
192  AGC AAC CAG GTA TTC CTC AAG ATC ACC AGT GTG GAC ACT GCA GAT ACT       396
193  Ser Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr
194                  100                 105                 110
195
196
197  GCC ACA TAC TAC TGT GCT CGA AGA GAG ACT GTG TTC TAC TGG TAC TTC       444
198  Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe
199                  115                 120                 125
200
201  GAT GTC TGG GGC GCA GGG ACC ACG GTC ACC GTC TCC TCA                   483
202  Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
203              130                 135                 140
204
205
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RAW SEQUENCE LISTING
PATENT APPLICATION   US/09/426,814

INPUT SET: S36192.raw

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206    (2)  INFORMATION FOR SEQ ID NO:4:
207
208          (i)  SEQUENCE CHARACTERISTICS:
209                 (A)  LENGTH: 140 amino acids
210                 (B)  TYPE: amino acid
211                 (D)  TOPOLOGY: linear
212
213         (ii)  MOLECULE TYPE: protein
214
215         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:4:
216
217    Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Leu Ile Val Pro Ala Tyr
218     1               5                  10                  15
219
220    Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
221             20                  25                  30
222
223    Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
224         35                  40                  45
225
226    Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
227        50                  55                  60
228
229    Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
230     65                  70                  75                  80
231
232    Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser
233                 85                  90                  95
234
235    Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala
236             100                 105                 110
237
238    Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp
239         115                 120                 125
240
241    Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
242         130                 135                 140
243
244
245    (2)  INFORMATION FOR SEQ ID NO:5:
246
247          (i)  SEQUENCE CHARACTERISTICS:
248                 (A)  LENGTH: 60 base pairs
249                 (B)  TYPE: nucleic acid
250                 (C)  STRANDEDNESS: double
251                 (D)  TOPOLOGY: unknown
252
253         (ii)  MOLECULE TYPE: cDNA
254
255         (ix)  FEATURE:
256                 (A)  NAME/KEY: CDS
257                 (B)  LOCATION: 1..60
258
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/426,814*

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Line   Error   Original Text

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION *US/09/426,814*

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< < THERE ARE NO ITEMS MISSING > >

SEQUENCE CORRECTION REPORT
PATENT APPLICATION   *US/09/426,814*

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Line	Original Text	Corrected Text